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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=3; day=10; hr=15; min=2; sec=27; ms=427;]

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Application No: 10554387 Version No: 2.0

Input Set:

Output Set:

Started: 2009-02-19 11:43:19.381
Finished: 2009-02-19 11:43:20.363
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 982 ms
Total Warnings: 11
Total Errors: 0
No. of SeqIDs Defined: 14
Actual SeqID Count: 14

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W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)

SEQUENCE LISTING

<110> Protalix Ltd.
 Shaaltiel, Yoseph
 Baum, Gideon
 Hashmueli, Sharon
 Lewkowitz, Ayala
 Bartfeld, Daniel

<120> PRODUCTION OF HIGH MANNOSE PROTEINS IN PLANT CULTURE

<130> 30570

<140> 10554387

<141> 2005-10-25

<150> IL 155588

<151> 2003-04-27

<150> PCT/IL2004/000181

<151> 2004-02-24

<160> 14

<170> PatentIn version 3.5

<210> 1

<211> 22

<212> PRT

<213> Artificial sequence

<220>

<223> ER signal peptide

<400> 1

Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
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Leu Ser Ser Ala Glu Phe
 20

<210> 2

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Vacuolar targeting signal from Tobacco chitinase A

<400> 2

Asp Leu Leu Val Asp Thr Met
 1 5

<210> 3
 <211> 21
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

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 cagaattcgc cgcgccctgc a 21

<210> 4
 <211> 22
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 4
 ctcagatctt ggcgatgcca ca 22

<210> 5
 <211> 19
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 5
 ctcagaagac cagagggct 19

<210> 6
 <211> 17
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Single strand DNA oligonucleotide

 <400> 6
 caaagcggcc atcgtgc 17

<210> 7
 <211> 1491
 <212> DNA
 <213> Homo sapiens

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<210> 8

<211> 496

<212> PRT

<213> Homo sapiens

<400> 8

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Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln
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Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr
260 265 270

His His Asn Val Arg Leu Leu Met Leu Asp Asp Gly Arg Leu Leu Leu
275 280 285

His Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val
290 295 300

His Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala Lys
305 310 315 320

Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu Phe
325 330 335

Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val Arg
340 345 350

Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr
355 360 365

Asn Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu
370 375 380

Asn Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro
385 390 395 400

Ile Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe
405 410 415

Tyr His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln Arg
420 425 430

Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala Leu
435 440 445

Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser Ser
450 455 460

Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu
465 470 475 480

Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln
485 490 495

<210> 9
<211> 338
<212> DNA
<213> Cauliflower mosaic virus

<400> 9
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ggaaaggcta tcgttcaaga tgcctctacc gacagtggtc ccaaagatgg acccccaccc 180
acgaggaaca tcgtggaaaa agaagacggt ccaaccacgt cttcaaagca agtggattga 240
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tcctctatat aaggaagttc atttcatttg gagaggac 338

<210> 10
<211> 66
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence encoding the ER signal peptide

<400> 10
atgaagacta atctttttct ctttctcatc ttttcacttc tcctatcatt atcctcggcc 60
gaattc 66

<210> 11
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Nucleic acid sequence encoding the vacuolar targeting sequence

<400> 11
gatcttttag tcgatactat g 21

<210> 12
<211> 167
<212> DNA

<213> Artificial sequence

<220>

<223> Nucleic acid sequence of the Agrobacterium tumefaciens terminator

<220>

<221> misc_feature

<222> (162)..(162)

<223> n is a, c, g, or t

<400> 12

taatttcatg atctgttttg ttgtattccc ttgcaatgca ggcctaggg ctatgaataa 60

agttaatgtg tgaatgtgtg aatgtgtgat tgtgacctga agggatcacg actataatcg 120

tttataataa acaaagactt tgtcccaaaa accccccccc cngcaga 167

<210> 13

<211> 2186

<212> DNA

<213> Artificial sequence

<220>

<223> nucleic acid sequence encoding high mannose human
glucocerebrosidase (GCD)

<220>

<221> misc_feature

<222> (2181)..(2181)

<223> n is a, c, g, or t

<400> 13

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ttcatcgaaa ggacagtaga aaaggaaggt ggctcctaca aatgccatca ttgcgataaa 120

ggaaaggcta tcgttcaaga tgctctacc gacagtggtc ccaaagatgg acccccaccc 180

acgaggaaca tcgtggaaaa agaagacggt ccaaccacgt cttcaaagca agtggattga 240

tgtgatatct ccaactgacgt aagggatgac gcacaatecc actatccttc gcaagaccct 300

tcctctatat aaggaagttc atttcatttg gagaggacag gcttcttgag atccttcaac 360

aattaccaac aacaacaaac aacaacaaac attacaatta ctatttacia ttacagtcga 420

gggatccaag gagatataac aatgaagact aatctttttc tctttctcat cttttcactt 480

ctcctatcat tatecteggc cgaattcgcc cgcccctgca tcctaaaag ctteggctac 540

agctcgggtg tgtgtgtctg caatgccaca tactgtgact cctttgaccc cccgaccttt 600

cctgcccttg gtaccttcag ccgctatgag agtacacgca gtgggcgacg gatggagctg 660

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atgtgtgatt gtgacctgaa gggatcacga ctataatcgt ttataataaa caaagacttt	2160
gtccccaaaa cccccccc ngcaga	2186

<210> 14

<211> 526

<212> PRT

<213> Artificial sequence

<220>

<223> High mannose human glucocerebrosidase (GCD)

<400> 14

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Leu Ser Ser Ala Glu Phe Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly
20 25 30

Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe
35 40 45

Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser
50 55 60

Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala
65 70 75 80

Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys
85 90 95

Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala
100 105 110

Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys
115 120 125

Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro
130 135 140

Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr
145 150 155 160

Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr
165 170 175

Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg
180 185 190

Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
195 200 205

Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly
 210 215 220

Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp
 225 230 235 240

Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn
 245 250 255

Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly
 260 265 270

Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro
 275 280 285

Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu Asp
 290 295 300

Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr Asp
 305 310 315 320

Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
 325 330 335

Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu
 340 345 350

Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys
 355 360 365

Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln
 370 375 380

Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp
 385 390 395 400

Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val
 405 410 415

Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr
 420 425 430

Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe
435 440 445

Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn
450 455 460

Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val
465 470 475 480

Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp
485 490 495

Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His
500 505 510

Thr Tyr Leu Trp His Arg Gln Asp Leu Leu Val Asp Thr Met
515 520 525